******************* (MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat May 13 09:58:28 2000; MasPar time 4.62 Seconds 230.882 Million cell updates/sec

Description:
Perfect Score:
Sequence:

Title:

>US-09-331-631-3 (29-73) from US09331631.pep (2 of 5) 361 1 SEFDRQEYEECKRQCMQLETSGQMRRCVSQCDKRFEEDIDWSKYD 45

Scoring table: PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 24.753; Variance 88.190; scale 0.281

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

21 23	, 154 187	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
; 72 71 71	77 73 73	361 361 259 109 97 95 95 95 77 77	Score
		100.0 100.0 711.7 26.9 26.3 26.3 221.3 221.3	Query Match
1416 1416 2703 2710	489 524 81 125	00000000000000000000000000000000000000	Length
			DB
W62835 R67358 R70236 W22482	W90341 W90339 Y12435 R13329 W81779	W62829 W62828 W62828 W62830 W62831 W62831 W62831 W62831 W6402831 W6	ID
Zea mays antimitorobial 2 Zea mays antimitorobial Human astrovirus serot P. falciparum Proj3. Plasmodium Proj3.	max SBP2 protein. max SBP1 protein. man 5' EST secrete 4 epididymis-speci man HE4 protein.	Macadamia integrifolia Macadamia integrifolia Macadamia integrifolia Macadamia integrifolia Gossypium hirsutum ant Theobroma cacao antimi Sequence encoded by 67 Human TSP1 protein. Human thrombospondin 1 Human concatamerised T Maize Id gene product. G. max truncated SBP2 Maize Id protein. G. max truncated SBP2	Description
3.166+01 3.90e+01 3.90e+01 4.77e+01 4.77e+01	1.39e+01 1.39e+01 3.18e+01 3.18e+01 3.18e+01	2.58 9.58e 9.96e 9.96e 9.96e 9.96e 1.26e 9.96e 1.26e 9.9	Pred. No.

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slit 3	mat	•	A thermophilic ligase		Homo sapiens B223 sequ	P. aeruginosa mucA.	Cyclic corticotrophin	(Cyclo 30-33)[D-Phe12,	Human transient recept	Mycobacterium species	ILTV thymidine kinase.	Mycobacterium species	Human type C lectin.	WD-40 domain-contg. Mu	Arabidopsis enhanced d	Antimicrobial maize pe	Zea mays antimicrobial	glycosy	N. gonorrhoeae glycosy	Human 5' EST secreted	Plasmodium var-7.
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ALIGNMENTS

RESULT ID W AC W DT 2 DE M KW :a KW :a KW :a FT P	Qu Be Ma Db	RESULPANCE OF THE STANCE OF TH
W62828 standard; Protein; 666 AA. W62828; 27-OCT-1998 (first entry) Macadamia integrifolia antimicrobial protein. 'antimicrobial protein; infestation; control. Key Rey Peptide 1. 28 //note= "signal peptide"	Query Match Query Match Query Match Sest Local Similarity 100.0%; Score 361; DB 1; Length 666; Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 29 SEFDRQEYEECKROCMQLETSGOMERCVSQCDKEFEEDIDWSKYD 73	162829 standard; Protein; 666 AA. 162829; 7-OCT-1998 (first entry) 10-Cation/Qualifiers 10-Cation/Qualifiers 10-EC 1996 (first entry) 10-EC 1997 (folia) 10-EC 1997 (foli

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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL
Bower NI, Goulter KC, Green JI
WPI; 98-377279/32.
                      W62832 standard; Protein; 590 AA.
W62832;
27-OCT-1998 (first entry)
Gossypium hirsutum antimicrobial protein.
antimicrobial protein; infestation; control.
Gossypium hirsutum.
w09827805-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for controlling microbial infestations of plants or mammal: claim 1; Page 43-45; 96pp; English.
The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian
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The sequence is that of an antimicrobial protein which
  02-JUL-1998
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Similarity 100.0%;
32; Conservative
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Green JL, Manners JM, Marcus JP;
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Pred. No. 9.96e-19;
0; Mismatches (
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No. 2.58e-30;
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07-JUN-1991; G00914.
11-JUN-1990; GB-013016.
(MRSC ) MARS UK LTD.
Spencer ME, Hodge R, Deakin E
WPI: 92-024418/03.
N-PSDB; Q20377.
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Novel anti-microbial protein from e.g. Macadamia integruseful for controlling microbial infestations of plants claim 1; Page 47-49; 96pp; English.

The sequence is that of an antimicrobial protein which microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R20181
R20181;
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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
BOWER NI, Goulter KC, Green JL, Manners JM, Mar
WPI; 98-377279/32.
                             expression vectors
Claim 4; Fig 2; 59
                                                                                                                                                                                                                                                                                                                                                                                  Theobroma cacao. WO9119801-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Cocoa; flavour; vicilin; seed storage protein.
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The sequence is that of an antimicrobial protein which cobe used to control microbial infestations in plants and
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                                                                                                                         Recombinant cocoa proteins - are
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Sequence encoded by 67 kD T. cacao protein cDNA
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20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
   Claim 4; Fig 2; 59pp; English
The inventors claim a 67 kD a
                                                                                           beans and produced
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16-JUL-1997, 112154.
16-JUL-1996; US-680845.
(MIXS/) MIXSON A J.
MIXSON AJ.
                                                                         R40823 stand
R40823;
R40823;
03-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the thrombospondin gene TSP1 which is used in a method to produce a cationic vehicle consisting of a cationic liposome: DNA complex where the DNA encodes an anti-angiogenic peptide or tumour suppressor protein. Such complexes are used for treatment of neoplastic and metabolic diseases especially for gene therapy of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TSP1 protein.
TSP1; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy;
liposome; DNA complex; tumour suppressor protein; treatment; neoplastic;
metabolic disease; tumour.
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W40287
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Human thrombospondin 1. hTSP-1; platelet glycoprotein; inhibitor; solid tumour; skin c
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Pred. No. 1.88e-01;
11; Mismatches 12
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Pred. No. 2.93e-01;
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cancer; angiogenic dysfunction;
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16-JUL-1996; US-680845.
(MIXS/) MIXSON A J.
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TSP1; thrombospondin; anti-angiogenic; cationic vehicle; gene
liposome; DNA complex; tumour suppressor protein; treatment;
metabolic disease; concatamer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W40288 standard; Protein; W40288; 18-AUG-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-FEB-1993; U01652.
24-FEB-1992; US-841656.
(NOUN ) UNIV NORTHWESTERN
BOUCK NP, Frazier WA, GC
                                                                                                                                                                                                                                                                                                             Complexes of DNA encoding anti-angiogenic peptide - with cationic liposome(s) or cationic polymer, useful for, e.g. gene therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
Misc_difference 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compsn. for inhibiting angiogenesis inhibitor comprising a peptide capal
                                                                                              Sequence
                                                                                                                                                                                                                                                                  Claim 9; Page 6-7; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; V10494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP-819758-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 93-288118/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
WO9316716-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanoma; diabetic retinopathy;
Kaposi's sarcoma; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vascularisation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSGQMRRC-VSQCDKRFEEDIDWS
                                                                                                                                                                                                                                                                                                                                                                                               98-078839/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 26.3%;
Similarity 50.0%;
12; Conservative
                                                                                                 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
383
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                       26.3%;
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.227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "encoded by GAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intervening sequence
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Score
Pred.
4; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 95; DB 1; Lei
Pred. No. 2.93e-01;
4; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
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                       No.
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    contg. a vascu
ble of inhibiting

                       DB 1; L
2.93e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cationic vehicle; gene therapy;
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                                           Length 441
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Peptides
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Conservative

Mismatches

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SSVQTRTCHIQECDKRFKQDGGWS
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TSGQMRRC-VSQCDKRFEEDIDWS

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RESULT
AC WAS SEEN OF THE COLOR OF THE COLOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T New isolated plant Id gene - used to develop prods. for use i altering the induction of flowering in plants

S Claim 7; Fig 3 and Fig 5; 58pp; English.

C The Id gene controls flower evocation in maize plants. The maize nucleic acid is similar to that of genes encoding zinc-

C finger regulatory proteins in animals.

C Transposons Ac and Ds constitute a family of related transpos celements present in maize. A derivative of Ds, Ds2, can be u to produce a new mutant of the Id gene. The Ds2 (in the present in the present constitute and inserted into the Id gene to produce id*.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                 New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds Claim 7; page 39-40; 58pp; English.

This sequence represents a novel sucrose binding protein, SBP2 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plant which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to produce a n of active Ac) and inserted i Sequence 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G. max truncated SBP2 protein.
SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
                                                                                                                                                                                                                                                                                                                                                                                     Chao WS, Grimes HD; WPI; 99-070155/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize;
Ds2; f
                                                                                                                                                                                                                                                                                                                                                                                                                    26-NOV-1998.
21-MAY-1998; U10465.
22-MAY-1997; US-047568.
(UNIW ) UNIV WASHINGTON STATE RES FOUND.
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31-OCT-1996.
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N-PSDB; T42174, T42175.
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WPI; 96-49762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAR-1997 (first
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16-MAR-1995; US-406186.
(COLD-) COLD SPRING HARBOR LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
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Zea mays; Id; id*; transposon; transposable element;
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Similarity 35.0%;
7; Conservative
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No.
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carbohydrate
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content
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Best Local
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Best Local
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18-FEB-1998; U03161.
30-DEC-1997; US-000640.
20-FEB-1997; US-804104.
(COLD-) COLD SPRING HARBOR LACCOLASANTI JJ, Sundaresan V;
WPI, 98-467564/40.
Chao wS, Grimes HD;
WPI; 99-070155/06.
New modified plant sucrose binding proteins -
transgenic plants which can have enhanced or d
uptake activity in developing seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Id gene controlling floral induction in maize - useful to create transgenic plants with earlier, delayed or inhibited floral induction e.g. to extend geographical range of crops Claim 5; Fig 3; 68pp; English.

The maize Id gene controls floral induction and is useful in the production of transgenic plants with altered floral induction times, i.e. earlier, delayed or inhibited floral induction. The Id gene and zinc-finger regulatory regions are useful to identify these genes in maize and isolate similar genes in other plants. The polypeptides and antibodies are also useful in Id detection e.g. to locate activity
                                                                                                                                                                                                                                                        Glycine max. W09853086-A1.
                                                                                                                                                                                                                                                                                                      24-MAY-1999 (first entry)
G. max truncated SBP1 protein.
SBP1; sucrose binding protein; SBP2; seed; carbohydrate content; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the seed (e.g. where the seed is the primary plant material harveste such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any
                                                                                                                                                 21-MAY-1998; U10465.
22-MAY-1997; US-047568.
(UNIW) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                     W90340;
                                                                                                                                                                                                                                                                                                                                                                                                                                       W90340 standard; protein;
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W09837201-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 GEKRWCCERCGKPYAVQSDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 21.3%;
Similarity 45.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               floral induction; transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           438 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.3%;
larity 35.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 438
                                                                                                                                                       STATE RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 77; DB 1; I
Pred. No. 1.39e+01;
6; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
6; M
                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                 SBP2; sucrose uptake; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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1.39e+01;
                                                decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 438;
                                                                      used to develop
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PI Chao WS, Grimes HD;

DR WFI; 99-070155/06.

PI New modified plant sucrose binding proteins - used to develop

PI transgenic plants which can have enhanced or decreased sucrose

PI uptake activity in developing seeds

CC laim 13D; Page 37-38; 58pp; English.

PS Claim 13D; Page 37-38; 58pp; English.

CC production of a modified plant sucrose binding protein, SBP2 isolated

CC from Glycine max. This protein is used in a method resulting in the

CC production of a modified plant sucrose binding protein (SBP) which has a

CC modified amino acid sequence compared to a corresponding wild-type SBP,

CC and where expression of the modified SBP in a yeast assay system confers

CC mhanced sucrose uptake compared to the corresponding wild-type SBP,

CC which have modified sucrose uptake activity in developing transgenic plants

CC seeds. Enhanced sucrose uptake activity in developing seeds may be

CC desirable where it is an advantage to increase the carbohydrate content

CC seeds might be desirable where the seed is the primary plant material harvested,

CC such as soybean). In contrast, decreased sucrose uptake activity in

CC such as soybean). In contrast, decreased sucrose uptake activity in

CC such as sybbean). In contrast, decreased sucrose uptake activity in

CC such as soybean). In contrast, decreased sucrose uptake activity in

CC such as soybean in developing seeds and so may be used to express any

CC such as soybean in developing seeds and so may be used to express any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 1
                                                                                                                                                                Query Match
Best Local :
                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 36-37; 58pp; English.

This sequence represents a novel sucrose binding protein, SBP1 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W90341 standard; protein; 489 W90341;
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-1998; U10465.
22-MAY-1997; US-047568.
(UNIW ) UNIV WASHINGTON STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycine max.
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39
                                42 CKHQCQQQRQYTESDKRTCLQQCD 65
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nes 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              max SBP2 protein
                                                                                                                                                                                                                                                                    489 AA;
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                                                                                                                            Conservative
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                                                                                                                     Score 77; DB 1; 1
Pred. No. 1.39e+01
6; Mismatches
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Pred. No. 1.39e+01;
6; Mismatches 6
60
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                                                                                                                                Indels
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Matches

Conservative

6;

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9

Indels

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2

Search completed: Sat May Job time: 9 secs.

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80 Db

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RESULT

AC W99

AC W99
                                                                                                                                                                                                                This sequence represents a novel sucrose binding protein, SBP1 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP.

The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be content of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any
Query Match
Best Local
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W90339 standard; protein; 524 AA.
W90339;
24-MAY-1999 (first entrv)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transgenic plants which can have enhanced uptake activity in developing seeds Disclosure; Page 34-36; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-1997; US-047568.
(UNIW ) UNIV WASHINGTON STATE RES FOUND Chao WS, Grimes HD;
WPI: 99-070155/06.
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SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
                                                                                                                                       transgene in developing seeds.
Sequence 524 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-NOV-1998; U10465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New modified plant sucrose binding proteins - used to develop
21.3%;
Similarity 44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     max
Score 77; DB 1; I
Pred. No. 1.39e+01;
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                                      Length 524;
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